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RAW SEQUENCE LISTING

DATE: 06/10/2003 P.6
TIME: 08:06:28

PATENT APPLICATION: US/09/747,155A

Input Set : D:\Breese-8.app

Output Set: N:\CRF4\06102003\I747155A.raw

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3 <110> APPLICANT: Rouquier, Sylvie
4   Giorgi, Dominique
6 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
8 <130> FILE REFERENCE: 19904-008
10 <140> CURRENT APPLICATION NUMBER: 09/747,155A
11 <141> CURRENT FILING DATE: 2000-12-21
13 <150> PRIOR APPLICATION NUMBER: 60/171,746
14 <151> PRIOR FILING DATE: 1999-12-22
16 <160> NUMBER OF SEQ ID NOS: 438
18 <170> SOFTWARE: PatentIn version 3.0
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21 <211> LENGTH: 649
22 <212> TYPE: DNA
23 <213> ORGANISM: Papio hamadryas
25 <220> FEATURE:
26 <221> NAME/KEY: misc_feature
27 <222> LOCATION: (1)..(649)
28 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA13; Accession DDBJ/EMBL/GenBank =
AF127814
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (2)..(649)
33 <223> OTHER INFORMATION: Product = olfactory receptor
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38   1           5           10          15
40 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc      97
41 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
42           20           25           30
44 cag gtc tat ttc tcc atg ttt ttt cct att ctg ggc aca cta ctc ctg      145
45 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu
46           35           40           45
48 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac      193
49 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
50           50           55           60
52 tat ata acc atc atg aac ccc cgc ctc tgt ggc ctc ctg gtt ttt gtc      241
53 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
54 65           70           75           80
56 acg tgg ctc att ggt gtc atg acg tcc ctc ctc cat att tct ctg atg      289
57 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
58           85           90           95
60 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc      337
61 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys

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62          100          105          110
64 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac      385
65 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
66          115          120          125
68 agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc      433
69 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
70          130          135          140
72 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag      481
73 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
74 145          150          155          160
76 atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct      529
77 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
78          165          170          175
80 cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
81 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
82          180          185          190
84 ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg      625
85 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
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89 Val Met Tyr Thr Val Val Thr Pro
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101 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA13; Accession DDBJ/EMBL/GenBank =
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109          20          25          30
112 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu
113          35          40          45
116 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
117          50          55          60
120 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
121 65          70          75          80
124 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
125          85          90          95
128 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
129          100          105          110
132 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
133          115          120          125
136 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
137          130          135          140

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140 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
141 145                      150                      155                      160
144 Met Ser Ser Ser Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
145                      165                      170                      175
148 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
149                      180                      185                      190
152 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
153                      195                      200                      205
156 Val Met Tyr Thr Val Val Thr Pro
157      210                      215

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160 <210> SEQ ID NO: 3

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167 <222> LOCATION: (1)..(642)

168 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA14; pseudogene; Accession

DDBJ/EMBL/GenBank = AF127815

170 <400> SEQUENCE: 3

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175 cgcatgtatg gaaagtctgc tcttggtgtg gatggcctat gaccggtttg tggccatctg      180
177 tcacccccta cactgcccag tcatcatgaa cccacgcctt tgtggctttt tagttttggt      240
179 gtctttttctt cttagcctgt tggattccca gctacacaat ttgattgtgt tacaacttac      300
181 ctgcttcaat gatgtggaaa tctctaaatt tttctgtgac ccttctcaac ttctcaatcc      360
183 tagcctgctc tgacacataa catagtcgta tattttattg gtaccataatt tggttttctt      420
185 cctctctcag ggatcctttt cttttactat aaaattgttt cctccattcc gagagttcgc      480
187 tcttcaggtg ggaagtataa agccttctcc acctgcagct ctcacctttc agttgtttgc      540
189 ttattttatg gaacagccct tggagggtac ctcagttcag ctgtctctct cccccccagg      600
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194 <210> SEQ ID NO: 4

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196 <212> TYPE: DNA

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200 <221> NAME/KEY: misc_feature

201 <222> LOCATION: (1)..(649)

202 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA15; Accession DDBJ/EMBL/GenBank = AF127816

204 <220> FEATURE:

205 <221> NAME/KEY: CDS

206 <222> LOCATION: (2)..(649)

207 <223> OTHER INFORMATION: Product = olfactory receptor

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212 1                      5                      10                      15
214 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc      97
215 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
216      20                      25                      30

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218 cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg      145
219 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
220          35          40          45
222 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac      193
223 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
224          50          55          60
226 tat ata acc atc atg aac ccc cgc ctc tgt ggc ctc ctg gtt ttt gtc      241
227 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
228 65          70          75          80
230 acg tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg      289
231 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
232          85          90          95
234 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc      337
235 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
236          100          105          110
238 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac      385
239 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
240          115          120          125
242 agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc      433
243 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
244          130          135          140
246 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag      481
247 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
248 145 :          150          155          160
250 atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct      529
251 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
252          165          170          175
254 cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
255 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
256          180          185          190
258 ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg      625
259 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
260          195          200          205
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264          210          215
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275 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA15; Accession DDBJ/EMBL/GenBank =
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283          20          25          30

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286 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
287      35      40      45
290 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
291      50      55      60
294 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
295 65      70      75      80
298 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
299      85      90      95
302 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
303      100     105     110
306 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
307      115     120     125
310 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
311      130     135     140
314 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
315 145     150     155     160
318 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
319      165     170     175
322 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
323      180     185     190
326 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
327      195     200     205
330 Val Met Tyr Thr Val Val Thr Pro
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342 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA; Accession DDBJ/EMBL/GenBank =

AF27817

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346 <222> LOCATION: (2)..(649)

347 <223> OTHER INFORMATION: Product = olfactory receptor

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352 1      5      10      15
354 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc      97
355 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
356      20      25      30
358 cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg      145
359 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
360      35      40      45
362 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tat cac tcc ctg cac      193
363 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His
364      50      55      60

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/747,155A

DATE: 06/10/2003
TIME: 08:06:29

Input Set : D:\Breese-8.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:433; N Pos. 12,18,27
Seq#:435; N Pos. 3,9,21
Seq#:437; N Pos. 4,22

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:3; Line(s) 168
Seq#:12; Line(s) 762
Seq#:21; Line(s) 1356
Seq#:22; Line(s) 1390
Seq#:23; Line(s) 1424
Seq#:24; Line(s) 1458
Seq#:25; Line(s) 1492
Seq#:26; Line(s) 1526
Seq#:27; Line(s) 1560
Seq#:28; Line(s) 1596
Seq#:29; Line(s) 1632
Seq#:30; Line(s) 1666
Seq#:31; Line(s) 1700
Seq#:36; Line(s) 2014
Seq#:37; Line(s) 2048
Seq#:40; Line(s) 2222
Seq#:41; Line(s) 2256
Seq#:42; Line(s) 2292
Seq#:43; Line(s) 2328
Seq#:52; Line(s) 2922
Seq#:53; Line(s) 2956
Seq#:58; Line(s) 3270
Seq#:59; Line(s) 3304
Seq#:60; Line(s) 3338
Seq#:61; Line(s) 3372
Seq#:64; Line(s) 3546
Seq#:66; Line(s) 3653
Seq#:67; Line(s) 3720
Seq#:72; Line(s) 4034
Seq#:73; Line(s) 4068
Seq#:76; Line(s) 4242
Seq#:81; Line(s) 4556
Seq#:88; Line(s) 5010
Seq#:111; Line(s) 6584
Seq#:114; Line(s) 6758
Seq#:117; Line(s) 6932

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : D:\Breese-8.app
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Seq#:118; Line(s) 6966
Seq#:119; Line(s) 7000
Seq#:120; Line(s) 7033
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Seq#:122; Line(s) 7101
Seq#:123; Line(s) 7135
Seq#:142; Line(s) 8429
Seq#:151; Line(s) 8975
Seq#:152; Line(s) 9005
Seq#:166; Line(s) 9774
Seq#:171; Line(s) 10060
Seq#:188; Line(s) 11009
Seq#:205; Line(s) 11967
Seq#:212; Line(s) 12345
Seq#:215; Line(s) 12492

VERIFICATION SUMMARY

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Input Set : D:\Breese-8.app

Output Set: N:\CRF4\06102003\I747155A.raw

L:25215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:433 after pos.:0

L:25256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:435 after pos.:0

L:25292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:437 after pos.:0

7